

I claim:

1. A method of determining the molecular flux rates of a plurality of proteins in all or a portion of the proteome of a cell, tissue or organism, said method comprising:
 - a. administering one or more isotope-labeled protein precursors to said cell, tissue or organism for a period of time sufficient for one or more isotope labels to be incorporated into a plurality of proteins in the proteome or portion thereof of the cell, tissue or organism;
 - b. obtaining the proteome or portion thereof from the cell, tissue, or organism;
 - c. identifying a plurality of mass isotopomeric envelopes of ions representing individual proteins in the proteome or portion of the proteome by mass spectrometry;
 - d. quantifying relative and absolute mass isotopomer abundances of ions within the mass isotopomeric envelope corresponding to each identified protein by mass spectrometry; and
 - e. calculating the molecular flux rates of each identified protein to determine the molecular flux rates of said plurality of proteins.
2. The method of claim 1, wherein said administering step (a) is continuous.
3. The method of claim 1, wherein said administering step (a) comprises administering said one or more protein precursors at regular measured intervals.
4. The method of claim 1, wherein said one or more protein precursors are administered orally.
5. The method of claim 1, further comprising modifying said proteins prior to said measuring step.
6. The method of claim 5, wherein said modifying comprises biochemically degrading said proteins to peptides or individual amino acids.
7. The method of claim 6, wherein said modifying comprises chemically altering said proteins.

8. The method of claim 1, wherein said identifying step (c) further comprises identifying individual proteins in the proteome or portion of the proteome by chromatography.
9. The method of claim 1, wherein said plurality of proteins comprises the proteome of said cell, tissue, or organism.
10. The method of claim 1, further comprising the step of displaying the rates of synthesis and degradation of said plurality of proteins.
11. The method of claim 1, wherein said one or more protein precursors comprise an amino acid.
12. The method of claim 11, wherein the one or more protein precursors are selected from the group consisting of H_2O , CO_2 , NH_3 , and HCO_3 .
13. The method of claim 1, wherein said isotope label is selected from the group consisting of ^2H , ^{13}C , ^{15}N , ^{18}O , ^{33}S and ^{34}S .
14. The method of claim 13, wherein said isotope is ^2H .
15. The method of claim 1, wherein said isotope-labeled protein precursor is selected from the group consisting of $^2\text{H}_2\text{O}$, H_2^{18}O , $^{13}\text{CO}_2$, $\text{C}^{18}\text{O}^{17}\text{O}$, H^{16}CO_3 , $^{15}\text{NH}_3$, ^2H -labeled amino acids, ^{13}C -labeled amino acids, ^{15}N -labeled amino acids, ^{18}O -labeled amino acids, ^{34}S -labeled amino acids, and ^{33}S -labeled amino acids.
16. The method of claim 15, wherein said isotope-labeled protein precursor is $^2\text{H}_2\text{O}$.
17. The method of claim 1, wherein the organism is a human.

18. The method of claim 1, comprising the additional step of discontinuing said administering step (a).
19. The method of claim 1, further comprising administering a diagnostic or therapeutic agent to said cell, tissue, or organism prior to said administering step (a).
20. A method of determining the effect of a diagnostic or therapeutic agent on a cell, tissue, or organism, comprising:
 - a. determining the molecular flux rates of a plurality of proteins in the cell, tissue, or organism according to the method of claim 1,
 - b. administering said agent; and
 - c. determining the molecular flux rates the plurality of proteins in the cell, tissue or organism according to the method of claim 1, to determine the effect of said diagnostic or therapeutic agent.
21. The method of claim 20, wherein said effect of a diagnostic or therapeutic agent on the molecular flux rates of the plurality of proteins in said cell, tissue or organism is used for the discovery, development or approval of a drug or other therapeutic agent.
22. A method of determining the effects of one or more genes on the molecular flux rates of a plurality of proteins in a cell, tissue, or organism, comprising:
 - a. determining the molecular flux rates a plurality of proteins in a first population of one or more cells, tissues, or organisms according to the method of claim 1, wherein said cells, tissues, or organisms of said first population comprise said one or more genes;
 - b. determining the molecular flux rates of the plurality of proteins in a second population of one or more cells, tissues, or organisms according to the method of claim 1, wherein said second population does not comprise said one or more genes;

- c. comparing the molecular flux rates in said first and second populations to determine the effect of one or more genes on the molecular flux rates of a plurality of proteins.
- 23. The method of claim 1, further comprising isolating a plurality of samples from said cell, tissue or organism.
- 24. A method of determining the molecular flux rates of a plurality of organic metabolites in all or a portion of the organeome of a cell, tissue or organism, said method comprising:
 - a. administering one or more isotope-labeled organic metabolites or organic metabolite precursors to said cell, tissue or organism for a period of time sufficient for one or more isotope labels from said one or more isotope-labeled organic metabolites to be incorporated into the a plurality of organic metabolites in the organeome or portion thereof of the cell, tissue or organism;
 - b. obtaining the organeome or portion thereof from the cell, tissue, or organism;
 - c. identifying a plurality of the mass isotopomeric envelopes of ions representing individual organic metabolites in the organeome or portion thereof by mass spectrometry;
 - d. quantifying relative and absolute mass isotopomer abundances of ions within the mass isotopomeric envelope corresponding to each organic metabolite identified in step (c) by mass spectrometry; and
 - e. calculating the rates of synthesis or removal of the identified organic metabolites to determine the rates of synthesis or removal of said plurality of organic metabolites.

25. The method of claim 24, wherein the one or more organic metabolites or organic metabolite precursors are selected from the group consisting of H_2O , CO_2 , NH_3 , HCO_3 , amino acids, monosaccharides, carbohydrates, lipids, fatty acids, nucleic acids, glycolytic intermediates, acetic acid, and tricarboxylic acid cycle intermediates.
26. The method of claim 24, wherein the isotope label is selected from the group consisting of ^2H , ^{13}C , ^{15}N , ^{18}O , ^{33}S or ^{34}S .
27. The method of claim 24, wherein said administering step (a) is continuous.
28. The method of claim 24, wherein said administering step (a) comprises administering said precursor at regular measured intervals.
29. The method of claim 24, wherein the one or more organic metabolites or organic metabolite precursors are administered orally.
30. The method of claim 24, comprising the additional step of discontinuing said administering step (a).
31. The method of claim 24, further comprising modifying said organic metabolites prior to said measuring step.
32. The method of claim 24, wherein said identifying step (c) further comprises identifying individual organic metabolites in the organeome or portion thereof by chromatography.
33. The method of claim 24, wherein said plurality of organic metabolites comprises the organeome of said cell, tissue, or organism.
34. The method of claim 24, further comprising the step of displaying the rates of synthesis or removal of said plurality of organic metabolites.
35. The method of claim 24, wherein the organic metabolite precursor is selected from the group consisting of H_2O , CO_2 , NH_3 , and HCO_3 .

36. The method of claim 26, wherein said isotope is ^2H .
37. The method of claim 35, wherein said organic metabolic precursor is H_2O .
38. The method of claim 24, wherein said isotope-labeled organic metabolite precursor is selected from the group consisting of $^2\text{H}_2\text{O}$, $^3\text{H}_2\text{O}$, and H_2^{18}O .
39. The method of claim 38, wherein said isotope-labeled organic metabolite precursor is $^2\text{H}_2\text{O}$.
40. The method of claim 24, wherein the organism is a human.
41. The method of claim 24, further comprising administering a diagnostic or therapeutic agent to said cell, tissue, or organism prior to said administering step (a).
42. A method of determining the effect of a diagnostic or therapeutic agent on a cell, tissue, or organism, comprising:
- determining the rates of synthesis or removal of a plurality of organic metabolites in the cell, tissue, or organism according to the method of claim 24,
 - administering said agent; and
 - determining the rates of synthesis or removal of the plurality of organic metabolites in the cell, tissue or organism according to the method of claim 24, to determine the effect of said diagnostic or therapeutic agent.
43. The method of claim 42, wherein said effect of a diagnostic or therapeutic agent on the rates of synthesis or removal of the plurality of organic metabolites in said

cell, tissue or organism is used for the discovery, development or approval of a drug or other therapeutic agent.

44. A method of determining the effects of one or more genes on the molecular flux rates of a plurality of organic metabolites in a cell, tissue, or organism, comprising:
- a. determining the molecular flux rates of a plurality of organic metabolites in a first population of one or more cells, tissues, or organisms according to the method of claim 24, wherein said cells, tissues, or organisms in said first population comprise said one or more genes;
 - b. determining the rates of synthesis or removal of the plurality of organic metabolites in a second population of one or more cells, tissues, or organisms according to the method of claim 24, wherein said second population does not comprise said one or more genes;
 - c. comparing the rates of synthesis or removal in said first and second populations to determine the effect of one or more genes on the rate of synthesis or removal of a plurality of organic metabolites.
45. The method of claim 1, further comprising isolating a plurality of samples from said cell, tissue or organism.
46. The rights to drugs or other therapeutic agents so discovered by the method of claim 21.
47. The rights to drugs or other therapeutic agents so discovered by the method of claim 43.